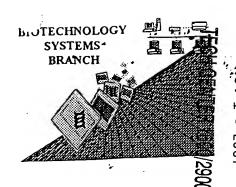# RAW SEQUENCE LISTING
ERROR REPORT

3617

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 09/596 444

Source: AU 1600

Date Processed by STIC: 10/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/596 444

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

1 ____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220>
Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RECEIVED
NOV 1 3 2001
GROUP 3600

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/596,444

DATE: 10/24/2001
TIME: 14:32:01

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

```
 3 <110> APPLICANT: Huang, Wei
 4       Hoekstra, Merl F
 5       Lee, Sandra K
 6       Cairns, Nicholas
 7       Kauvar, Lawrence M
 8       Sportsman, J Richard
10 <120> TITLE OF INVENTION: PHOSPHORYLATION ASSAYS
12 <130> FILE REFERENCE: LJL 354B
14 <140> CURRENT APPLICATION NUMBER: US 09/596,444
15 <141> CURRENT FILING DATE: 2000-06-19
17 <160> NUMBER OF SEQ ID NOS: 48
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 10
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <221> NAME/KEY: MOD_RES
28 <222> LOCATION: (5)..(5)
29 <223> OTHER INFORMATION: PHOSPHORYLATION
32 <220> FEATURE:
33 <221> NAME/KEY: MOD_RES
34 <222> LOCATION: (10)..(10)
35 <223> OTHER INFORMATION: BIOTINYLATION
38 <400> SEQUENCE: 1
40 Gly Glu Glu Gly Tyr Met Pro Met Gly Lys
41 1               5                   10
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 17
46 <212> TYPE: PRT
47 <213> ORGANISM: Artificial
49 <220> FEATURE:
50 <221> NAME/KEY: MOD_RES
51 <222> LOCATION: (1)..(1)
52 <223> OTHER INFORMATION: BIOTINYLATION
55 <220> FEATURE:
56 <221> NAME/KEY: MOD_RES
57 <222> LOCATION: (1)..(1)
58 <223> OTHER INFORMATION: AMIDATION
61 <400> SEQUENCE: 2
63 Glu Gly Pro Trp Leu Glu Glu Glu Glu Glu Ala Tyr Gly Trp Met Asp
64 1               5                   10                  15
67 Phe
71 <210> SEQ ID NO: 3
72 <211> LENGTH: 8
73 <212> TYPE: PRT
74 <213> ORGANISM: Artificial
```

C--> (lines 24, 47, 74)

Handwritten annotations:

Errored: A 213 response of "Artificial" requires an explanation in field 223.
FYI: "Artificial Sequence" is the preferred response. MH

A field 223 explanation is mandatory

Does Not Comply
Corrected Diskette Needed

RECEIVED
NOV 1 3 2001
GROUP 3600

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
            RAW SEQUENCE LISTING              DATE: 10/24/2001
            PATENT APPLICATION:  US/09/596,444   TIME: 14:32:01

            Input Set : A:\Sequence Listing.txt.txt
            Output Set: N:\CRF3\10242001\I596444.raw

W--> 76 <220> FEATURE:
W--> 76 <223> OTHER INFORMATION:
     76 <400> SEQUENCE: 3
     78 Asp Tyr Met Thr Met Gln Ile Gly
     79 1               5
     82 <210> SEQ ID NO: 4
     83 <211> LENGTH: 11
     84 <212> TYPE: PRT
C--> 85 <213> ORGANISM: Artificial
W--> 87 <220> FEATURE:
W--> 87 <223> OTHER INFORMATION:
     87 <400> SEQUENCE: 4
     89 Ser Arg Gly Asp Tyr Met Thr Met Gln Ile Gly
     90 1               5                   10
     93 <210> SEQ ID NO: 5
     94 <211> LENGTH: 11
     95 <212> TYPE: PRT
C--> 96 <213> ORGANISM: Artificial
W--> 98 <220> FEATURE:
W--> 98 <223> OTHER INFORMATION:
     98 <400> SEQUENCE: 5
    100 Glu Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu
    101 1               5                   10
    104 <210> SEQ ID NO: 6
    105 <211> LENGTH: 10
    106 <212> TYPE: PRT
C--> 107 <213> ORGANISM: Artificial
    109 <220> FEATURE:
    110 <221> NAME/KEY: MOD_RES
    111 <222> LOCATION: (5)..(5)
    112 <223> OTHER INFORMATION: PHOSPHORYLATION
    115 <400> SEQUENCE: 6
    117 Glu Lys Arg Pro Ser Arg Ser Lys Tyr Leu
    118 1               5                   10
    121 <210> SEQ ID NO: 7
    122 <211> LENGTH: 10
    123 <212> TYPE: PRT
C--> 124 <213> ORGANISM: Artificial
    126 <220> FEATURE:
    127 <221> NAME/KEY: MOD_RES
    128 <222> LOCATION: (8)..(8)
    129 <223> OTHER INFORMATION: PHOSPHORYLATION
    132 <400> SEQUENCE: 7
    134 Glu Lys Arg Pro Ser Gln Arg Ser Tyr Leu
    135 1               5                   10
    138 <210> SEQ ID NO: 8
    139 <211> LENGTH: 9
    140 <212> TYPE: PRT
C--> 141 <213> ORGANISM: Artificial
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     144 <221> NAME/KEY: MOD_RES
     145 <222> LOCATION: (5)..(5)
     146 <223> OTHER INFORMATION: PHOSPHORYLATION
     149 <220> FEATURE:
     150 <221> NAME/KEY: MOD_RES
     151 <222> LOCATION: (7)..(7)
     152 <223> OTHER INFORMATION: PHOSPHORYLATION
     155 <400> SEQUENCE: 8
     157 Glu Lys Arg Pro Ser Arg Ser Tyr Leu
     158 1               5
     161 <210> SEQ ID NO: 9
     162 <211> LENGTH: 14
     163 <212> TYPE: PRT
C--> 164 <213> ORGANISM: Artificial
     166 <220> FEATURE:
     167 <221> NAME/KEY: MOD_RES
     168 <222> LOCATION: (11)..(11)
     169 <223> OTHER INFORMATION: PHOSPHORYLATION
     172 <400> SEQUENCE: 9
     174 Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg Lys
     175 1               5                   10
     178 <210> SEQ ID NO: 10
     179 <211> LENGTH: 11
     180 <212> TYPE: PRT
C--> 181 <213> ORGANISM: Artificial
     183 <220> FEATURE:
     184 <221> NAME/KEY: MOD_RES
     185 <222> LOCATION: (7)..(7)
     186 <223> OTHER INFORMATION: PHOSPHORYLATION
     189 <400> SEQUENCE: 10
     191 Lys His Phe Pro Gln Phe Ser Tyr Ser Ala Ser
     192 1               5                   10
     195 <210> SEQ ID NO: 11
     196 <211> LENGTH: 11
     197 <212> TYPE: PRT
C--> 198 <213> ORGANISM: Artificial
     200 <220> FEATURE:
     201 <221> NAME/KEY: MOD_RES
     202 <222> LOCATION: (1)..(1)
     203 <223> OTHER INFORMATION: PHOSPHORYLATION
     206 <400> SEQUENCE: 11
     208 Ser Pro Glu Leu Glu Arg Leu Ile Ile Gln Cys
     209 1               5                   10
     212 <210> SEQ ID NO: 12
     213 <211> LENGTH: 11
     214 <212> TYPE: PRT
C--> 215 <213> ORGANISM: Artificial
     217 <220> FEATURE:
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```
218 <221> NAME/KEY: MOD_RES
219 <222> LOCATION: (9)..(9)
220 <223> OTHER INFORMATION: PHOSPHORYLATION
223 <220> FEATURE:
224 <221> NAME/KEY: MOD_RES
225 <222> LOCATION: (11)..(11)
226 <223> OTHER INFORMATION: PHOSPHORYLATION
229 <400> SEQUENCE: 12
231 Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
232 1               5                   10
235 <210> SEQ ID NO: 13
236 <211> LENGTH: 11
237 <212> TYPE: PRT
C--> 238 <213> ORGANISM: Artificial
240 <220> FEATURE:
241 <221> NAME/KEY: MOD_RES
242 <222> LOCATION: (6)..(6)
243 <223> OTHER INFORMATION: PHOSPHORYLATION
246 <400> SEQUENCE: 13
248 Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
249 1               5                   10
252 <210> SEQ ID NO: 14
253 <211> LENGTH: 5
254 <212> TYPE: PRT
C--> 255 <213> ORGANISM: Artificial
257 <220> FEATURE:
258 <221> NAME/KEY: MOD_RES
259 <222> LOCATION: (2)..(2)
260 <223> OTHER INFORMATION: PHOSPHORYLATION
263 <400> SEQUENCE: 14
265 Leu Thr Pro Leu Lys
266 1               5
269 <210> SEQ ID NO: 15
270 <211> LENGTH: 5
271 <212> TYPE: PRT
C--> 272 <213> ORGANISM: Artificial
274 <220> FEATURE:
275 <221> NAME/KEY: MOD_RES
276 <222> LOCATION: (2)..(2)
277 <223> OTHER INFORMATION: PHOSPHORYLATION
280 <400> SEQUENCE: 15
282 Phe Thr Pro Leu Gln
283 1               5
286 <210> SEQ ID NO: 16
287 <211> LENGTH: 8
288 <212> TYPE: PRT
C--> 289 <213> ORGANISM: Artificial
291 <220> FEATURE:
292 <221> NAME/KEY: MOD_RES
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```
                    RAW SEQUENCE LISTING          DATE: 10/24/2001
                    PATENT APPLICATION:  US/09/596,444    TIME: 14:32:01

                    Input Set : A:\Sequence Listing.txt.txt
                    Output Set: N:\CRF3\10242001\I596444.raw

     293 <222> LOCATION: (4)..(4)
     294 <223> OTHER INFORMATION: PHOSPHORYLATION
     297 <400> SEQUENCE: 16
     299 Arg Lys Arg Thr Leu Arg Arg Leu
     300 1               5
     303 <210> SEQ ID NO: 17
     304 <211> LENGTH: 7
     305 <212> TYPE: PRT
C--> 306 <213> ORGANISM: Artificial
     308 <220> FEATURE:
     309 <221> NAME/KEY: MOD_RES
     310 <222> LOCATION: (5)..(5)
     311 <223> OTHER INFORMATION: PHOSPHORYLATION
     314 <400> SEQUENCE: 17
     316 Leu Arg Arg Ala Ser Leu Gly
     317 1               5
     320 <210> SEQ ID NO: 18
     321 <211> LENGTH: 12
     322 <212> TYPE: PRT
C--> 323 <213> ORGANISM: Artificial
     325 <220> FEATURE:
     326 <221> NAME/KEY: MOD_RES
     327 <222> LOCATION: (8)..(8)
     328 <223> OTHER INFORMATION: PHOSPHORYLATION
     331 <400> SEQUENCE: 18
     333 Lys Lys Leu Asn Arg Thr Leu Ser Val Ala Ser Leu
     334 1               5                   10
     337 <210> SEQ ID NO: 19
     338 <211> LENGTH: 7
     339 <212> TYPE: PRT
C--> 340 <213> ORGANISM: Artificial
     342 <220> FEATURE:
     343 <221> NAME/KEY: MOD_RES
     344 <222> LOCATION: (6)..(6)
     345 <223> OTHER INFORMATION: PHOSPHORYLATION
     348 <220> FEATURE:
     349 <221> NAME/KEY: MOD_RES
     350 <222> LOCATION: (7)..(7)
     351 <223> OTHER INFORMATION: AMIDATION
     354 <400> SEQUENCE: 19
     356 Arg Pro Arg Ala Ala Thr Phe
     357 1               5
     360 <210> SEQ ID NO: 20
     361 <211> LENGTH: 7
     362 <212> TYPE: PRT
C--> 363 <213> ORGANISM: Artificial
     365 <220> FEATURE:
     366 <221> NAME/KEY: MOD_RES
     367 <222> LOCATION: (5)..(5)
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VERIFICATION SUMMARY   DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444   TIME: 14:32:02

Input Set : **A:\Sequence Listing.txt.txt**
Output Set: **N:\CRF3\10242001\I596444.raw**

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L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:47 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:74 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:76 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:76 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:85 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:87 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:87 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:96 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:98 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:98 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:124 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:141 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:164 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:181 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:198 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:238 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:255 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:272 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:289 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:306 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:340 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:363 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:386 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:421 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:462 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:497 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:520 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:537 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:566 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:601 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:630 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:647 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:664 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:681 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:698 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:715 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:717 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:717 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:726 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:728 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:728 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:737 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:739 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:739 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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VERIFICATION SUMMARY   DATE: 10/24/2001
PATENT APPLICATION: US/09/596,444   TIME: 14:32:02

Input Set : A:\Sequence Listing.txt.txt
Output Set: N:\CRF3\10242001\I596444.raw

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L:750 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:750 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:759 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:761 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:761 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:770 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:772 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:772 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:781 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:783 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:783 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:792 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:794 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:794 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:803 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:805 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:805 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:814 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:816 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:816 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:825 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:827 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:827 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:836 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:838 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:838 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:847 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:849 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:849 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:858 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:875 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
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